



FIGURE 1A

Amino acid sequence for full-length human wild type AKT3 [SEQ. ID No. 1]
(Residues 136-461 are underlined)

MSDVTIVKEG WVQKRGEYIK NWRPRYFLLK TDGSFIGYKE KPQDVDPYP LNNFSVAKCQ	60
LMKTERPKPN TFIIRCLQWT TVIERTFHVD TPEEREWE AIQAVADRLQ RQEEREMNCS	120
PTSQIDNIGE EEMDASTTHH KRKTMDFDY LKLLGKGTFG KVILVREKAS GKYYAMKILK	180
KEVIIAKDEV AHTLTESRVL KNTRHPFLTS LKYSFQTKDR LCFVMEYVNG GELFFHLSRE	240
RVFSEDRTRF YGAEIVSALD YLHSGKIVYR DLKLENLMLD KDGHIKITDF GLCKEGITDA	300
ATMKTFCGTP EYLAPEVLED NDYGRAVDWW GLGVVVMYEMM CGRLPFYNQD HEKLFELILM	360
EDIKFPTTLS SDAKSLLSGL LIKDPNKRLG GGPDDAKEIM RHSFFSGVNW QDVYDKKLVP	420
PFKPQVTSET DTRYFDEEFT AQTITITPPE KYDEDGMDCM DNERRPHFPQ FSYSASGRE	479

Human cDNA sequence encoding residues 136-461 of AKT3 [SEQ. ID No. 2]

TCTACAACCC ATCATAAAAG AAAGACAATG AATGATTTTG ACTATTTGAA ACTACTAGGT	60
AAAGGCAC TTGGGAAAGT TATTTGGTT CGAGAGAAGG CAAGTGGAAA ATACTATGCT	120
ATGAAGATTG TGAAGAAAGA AGTCATTATT GCAAAGGATG AAGTGGCACA CACTCTAACT	180
GAAAGCAGAG TATTAAGAA CACTAGACAT CCCTTTTAA CATCCTTGAA ATATTCTTC	240
CAGACAAAAG ACCGTTGTG TTTTGTGATG GAATATGTTA ATGGGGCGA GCTGTTTTC	300
CATTTGTCGA GAGAGCGGGT GTTCTCTGAG GACCGCACAC GTTCTATGG TGCAGAAATT	360
GTCTCTGCCT TGGACTATCT ACATTCGGGA AAGATTGTGT ACCGTGATCT CAAGTTGGAG	420
AATCTAATGC TGGACAAAGA TGGCCACATA AAAATTACAG ATTTTGGACT TTGCAAAGAA	480
GGGATCACAG ATGCAGCCAC CATGAAGACA TTCTGTGGCA CTCCAGAATA TCTGGCACCA	540
GAGGTGTTAG AAGATAATGA CTATGCCGA GCAGTAGACT GGTGGGGCCT AGGGGTTGTC	600
ATGTATGAAA TGATGTGTGG GAGGTTACCT TTCTACAACC AGGACCATGA GAAACTTTT	660
GAATTAATAT TAATGGAAGA CATTAAATT CCTCGAACAC TCTCTTCAGA TGCAAATCA	720
TTGCTTCAG GGCTCTTGAT AAAGGATCCA ATAACACGCC TTGGTGGAGG ACCAGATGAT	780
GCAAAAGAAA TTATGAGACA CAGTTCTTC TCTGGAGTAA ACTGGCAAGA TGTATATGAT	840
AAAAAGCTTG TACCTCCTT TAAACCTCAA GTAACATCTG AGACAGATAC TAGATATTT	900
GATGAAGAAT TTACAGCTCA GACTATTACA ATAACACCAC CTGAAAAATA TGATGAGGAT	960
GGTATGGACT GCATGGAC	978

FIGURE 1B

**Amino acid sequence for residues 136-461 of AKT3 with a cleavable
N-terminal intein tag [SEQ. ID No. 3]**

**(N-terminal intein tag and cleavage site are underlined. The intein tag was
subsequently cleaved resulting in CRSL (residues 227-230 of SEQ. ID No. 3) fused
to the N-terminal of amino acids 136-461 of SEQ. ID No. 1)**

MKIEEGKLTN PGVSAWQVNT AYTAGQLVTY NGKTYKCLQP HTSLAGWEPS NVPALWQLQN	60
NGNNNGLELRE SGAISGDSLI SLASTGKRVS IKDLLDEKDF EIWAINEQTM KLESAKVSRV	120
FCTGKKLVYI LKTRLGRTIK ATANHRLFTI DGWKRRLDELS LKEHIALPRK LESSSLQLSP	180
EIEKLSQSDI YWDSIVSITR TGVEEVFDLT VPGPHNFVAN DIIVHNCRSL STTHHKRKT	240
NDFDYLKLLG KGTGKVILV REKASGKYYA MKILKKEVII AKDEVAHTLT ESRVLKNTRH	300
PFLTSLKYSF QTKDRLCFVM EYVNGGELFF HLSRERVFSE DRTRFYGAEI VSALDYLHSG	360
KIVYRDLKLE NLMMDKDGHI KITDFGLCKE GITDAATMKT FCGTPEYLAP EVLEDNDYGR	420
AVDWWGLGVV MYEMMCGRGP FYNQDHEKLF ELILMEDIKF PRTLSSDAKS LLSSGLLIKDP	480
NKRLGGGPDD AKEIMRHSFF SGVNWQDVYD KKLVPPFKPQ VTSETDTRYF DEEFTAQQTIT	540
ITPPEKYDED GMDCMD	556

**Amino acid sequence for residues 227-556 of SEQ. ID No. 3
[SEQ. ID No. 4]**

CRSLSTTHHK RKTMDFDYL KLLGKGTFGK VILVREKASG KYYAMKILKK EVIIAKDEVA	60
HTLTERVVLK NTRHPFLTSI KYSFQTKDRL CFVMEYVNGG ELFFHLSRER VFSEDRTRFY	120
GAEIVSALDY LHSRKIVYRD LKLENLMLDK DGHIKITDFG LCKEGITDAA TMKTFCGTPE	180
YLAPEVLEDN DYGRAVDWWG LGVVMYEMMC GRLPFYNQDH EKLFELILME DIKFPTLSS	240
DAKSLLSGLL IKDPNKRLLGG GPDDAKEIMR HSFFSGVNWQ DVYDKKLVPP FKPQVTSETD	300
TRYFDEEFTA QTITITPPEK YDEDGMDCMD	360

FIGURE 5

